

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, YI
FLEISCHMANN, ROBERT
- (ii) TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/424,424
 - (B) FILING DATE: 21-APR-1995
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Michele M. Wales
 - (B) REGISTRATION NUMBER: 43,975
 - (C) REFERENCE/DOCKET NUMBER: PF116
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (301) 309-8504
 - (B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 266..2446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGGCAGG GAGTGAGGAG CGAGCGGAGT CGCGTGC GCC GCGCGAGCT CCGGGTCGCC 60

CCAGCCCCAG CCGGGGGCCT GTGGCGGGGG AGGAGCTGTG CGTCCGCAC CCGTCGGGAT 120

CGCAGCTGCT	CGGCCGGAGT	GCACGGGCCG	AGTCTGGCGC	ACTACCCACG	CGTGACAGGT		180										
CCCTGAATGA	GAAGGAGCTG	ACAGCAGCTG	AATTCATCT	TCTCTGTGTG	CTGGGGAGCA		240										
GGGCTACACG	GCCCAGGTGG	CATCA	ATG	CCG	AAG	AAC	AGC	AAA	GTG	ACC	CAG		292				
			Met	Pro	Lys	Asn	Ser	Lys	Val	Thr	Gln						
			1				5										
CGT	GAG	CAC	AGC	AGT	GAG	CAT	GTC	ACT	GAG	TCC	GTG	GCC	GAC	CTG	CTG		340
Arg	Glu	His	Ser	Ser	Glu	His	Val	Thr	Glu	Ser	Val	Ala	Asp	Leu	Leu		
10				15						20				25			
GCC	CTC	GAG	GAG	CCT	GTG	GAC	TAT	AAG	CAG	AGT	GTA	CTG	AAT	GTG	GCT		388
Ala	Leu	Glu	Glu	Pro	Val	Asp	Tyr	Lys	Gln	Ser	Val	Leu	Asn	Val	Ala		
				30					35					40			
GGT	GAG	GCA	GGC	GGC	AAG	CAG	AAG	GCG	GTG	GAG	GAG	GAG	CTG	GAT	GCA		436
Gly	Glu	Ala	Gly	Gly	Lys	Gln	Lys	Ala	Val	Glu	Glu	Glu	Leu	Asp	Ala		
			45					50					55				
GAG	GAC	CGG	CCG	GCC	TGG	AAC	AGT	AAG	CTG	CAG	TAC	ATC	CTG	GCC	CAG		484
Glu	Asp	Arg	Pro	Ala	Trp	Asn	Ser	Lys	Leu	Gln	Tyr	Ile	Leu	Ala	Gln		
		60					65					70					
ATT	GGC	TTC	TCT	GTG	GGC	CTC	GGC	AAC	ATC	TGG	AGG	TTC	CCC	TAC	CTG		532
Ile	Gly	Phe	Ser	Val	Gly	Leu	Gly	Asn	Ile	Trp	Arg	Phe	Pro	Tyr	Leu		
	75					80					85						
TGC	CAG	AAA	AAT	GGA	GGA	GGT	GCT	TAC	CTG	GTG	CCC	TAC	CTG	GTG	CTG		580
Cys	Gln	Lys	Asn	Gly	Gly	Gly	Ala	Tyr	Leu	Val	Pro	Tyr	Leu	Val	Leu		
90					95					100				105			
CTG	ATC	ATC	ATC	GGG	ATC	CCC	CTC	TTC	TTC	CTG	GAG	CTG	GCT	GTG	GGT		628
Leu	Ile	Ile	Ile	Gly	Ile	Pro	Leu	Phe	Phe	Leu	Glu	Leu	Ala	Val	Gly		
				110					115					120			
CAG	AGG	ATC	CGC	CGC	GGA	AGC	ATC	GGT	GTG	TGG	CAC	TAT	ATA	TGT	CCC		676
Gln	Arg	Ile	Arg	Arg	Gly	Ser	Ile	Gly	Val	Trp	His	Tyr	Ile	Cys	Pro		
			125					130					135				
CGC	CTG	GGG	GGG	ATC	GGC	TTC	TCC	AGC	TGC	ATA	GTC	TGT	CTC	TTT	GTG		724
Arg	Leu	Gly	Gly	Ile	Gly	Phe	Ser	Ser	Cys	Ile	Val	Cys	Leu	Phe	Val		
			140				145					150					
GGG	CTG	TAT	TAT	AAT	GTG	ATC	ATC	GGG	TGG	AGC	ATC	TTC	TAT	TTC	TTC		772
Gly	Leu	Tyr	Tyr	Asn	Val	Ile	Ile	Gly	Trp	Ser	Ile	Phe	Tyr	Phe	Phe		
	155				160						165						
AAG	TCC	TTC	CAG	TAC	CCG	CTG	CCC	TGG	AGT	GAA	TGT	CCT	GTC	GTC	AGG		820
Lys	Ser	Phe	Gln	Tyr	Pro	Leu	Pro	Trp	Ser	Glu	Cys	Pro	Val	Val	Arg		
170				175						180					185		
AAT	GGG	AGC	GTC	GCA	GTG	GTG	GAG	GCA	GAG	TGT	GAA	AAG	AGC	TCA	GCC		868
Asn	Gly	Ser	Val	Ala	Val	Val	Glu	Ala	Glu	Cys	Glu	Lys	Ser	Ser	Ala		
				190					195					200			
ACT	ACC	TAC	TTC	TGG	TAC	CGA	GAG	GCT	TTG	GAC	ATC	TCT	GAC	TCC	ATC		916
Thr	Thr	Tyr	Phe	Trp	Tyr	Arg	Glu	Ala	Leu	Asp	Ile	Ser	Asp	Ser	Ile		
			205					210					215				
TCG	GAG	AGT	GGG	GGC	CTC	AAC	TGG	AAG	ATG	ACC	CTG	TGC	CTC	CTC	GTG		964
Ser	Glu	Ser	Gly	Gly	Leu	Asn	Trp	Lys	Met	Thr	Leu	Cys	Leu	Leu	Val		
		220					225					230					

TGC Val	TGG Trp	AGC Ser	ATC Ile	GGG Gly	GGG Gly	ATG Met	GCT Ala	GTC Val	GGT Gly	AAG Lys	GGC Gly	ATC Ile	CAG Gln	TCC Ser	TCG Ser	1012
235						240					245					
GGG Gly	AAG Lys	GTG Val	ATG Met	TAT Tyr	TTC Phe	AGC Ser	TCC Ser	CTC Leu	TTC Phe	CCC Pro	TAC Tyr	GTG Val	GTG Val	CTG Leu	GCC Ala	1060
250					255					260					265	
TGC Cys	TTC Phe	CTG Leu	GTC Val	CGG Arg	GGG Gly	TTG Leu	TTG Leu	TTG Leu	CGA Arg	GGG Gly	GCA Ala	GTT Val	GAT Asp	GGC Gly	ATC Ile	1108
				270					275					280		
CTA Leu	CAC His	ATG Met	TTC Phe	ACT Thr	CCC Pro	AAG Lys	CTG Leu	GTC Val	AAG Lys	ATG Met	CTG Leu	GAC Asp	CCC Pro	CAG Gln	GTG Val	1156
				285				290					295			
TGG Trp	CGG Arg	GAG Glu	GTA Val	GCT Ala	ACC Thr	CAG Gln	GTC Val	TTT Phe	GGC Gly	TTG Leu	GGT Leu	CTG Gly	GGC Gly	TTT Phe		1204
		300				305					310					
GGT Gly	GGT Gly	GTC Val	ATT Ile	GTC Val	TTC Phe	TCC Ser	AGT Ser	TAC Tyr	AAT Asn	AAG Lys	CAG Gln	GAC Asp	AAC Asn	AAC Asn	TGC Cys	1252
315						320					325					
CAC His	TTC Phe	GAT Asp	GGC Gly	GCC Ala	CTG Val	GTG Val	TCC Ser	TTC Phe	ATC Ile	AAC Asn	TTC Phe	TTC Phe	ACG Thr	TCA Ser	GTG Val	1300
330				335						340					345	
TTG Leu	GCC Ala	ACC Thr	CTC Leu	GTG Val	GTG Val	TTT Phe	GTT Val	GTT Val	TTG Leu	GGC Gly	TTC Phe	AAG Lys	GCC Ala	AAC Asn	ATC Ile	1348
				350					355					360		
ATG Met	AAT Asn	GAG Glu	AAG Lys	TGT Cys	GTG Val	GTC Val	GAG Glu	AAT Asn	GCT Ala	GAG Glu	AAA Lys	ATC Ile	CTA Leu	GGG Gly	TAC Tyr	1396
			365					370					375			
CTT Leu	AAC Asn	ACC Thr	AAC Asn	GTC Val	CTG Leu	AGC Ser	CGG Arg	GAC Asp	CTC Leu	ATC Ile	CCA Pro	CCC Pro	CAC His	GTC Val	AAC Asn	1444
		380					385					390				
TTC Phe	TCC Ser	CAC His	CTG Leu	ACC Thr	ACA Thr	AAG Lys	GAC Asp	TAC Tyr	ATG Met	GAG Glu	ATG Met	GAC Met	AAT Asn	GTC Val	ATC Ile	1492
	395					400					405					
ATG Met	ACC Thr	GTG Val	AAG Lys	GAG Glu	GAC Asp	CAG Gln	TTC Phe	TCA Ser	GCC Ala	CTG Leu	GGC Gly	CTT Leu	GAC Asp	CCC Pro	TGC Cys	1540
410				415						420					425	
CTT Leu	CTG Leu	GAG Glu	GAC Asp	GAG Glu	CTG Leu	GAC Asp	AAG Lys	TCC Ser	GTG Val	CAG Gln	GGC Gly	ACA Thr	GGC Gly	CTG Leu	GCC Ala	1588
			430						435					440		
TTC Phe	ATC Ile	GCC Ala	Phe	ACT Thr	GAG Glu	GCC Ala	ATG Met	ACG Thr	CAC His	CTC Phe	CCC Pro	ACC Thr	TCC Ser	CCG Pro	TTC Phe	1636
			445					450					455			
TGG Trp	TCC Ser	GTC Val	ATG Met	TTC Phe	TTC Phe	TTG Leu	ATG Met	CTT Leu	ATC Ile	AAC Asn	CTG Leu	GGC Gly	CTG Leu	GGC Gly	AGC Ser	1684
		460					465				470					
ATG Met	ATC Ile	GGG Gly	ACC Thr	ATG Met	GCA Ala	GGC Gly	ATC Ile	ACC Thr	ACG Thr	CCC Pro	ATC Ile	GAC Ile	ATC Asp	GAC Thr	TCC Ser	1732

475				480				485								
AAG Lys 490	GTG Val	CCC Pro	AAG Lys	GAG Glu	ATG Met 495	TTC Phe	ACA Thr	GTG Val	GGC Gly	TGC Cys 500	TGT Cys	GTC Val	TTT Phe	ACA Thr	TTC Phe 505	1780
CTC Leu	GTG Val	GGA Gly	CTG Leu	TTG Leu 510	TTC Phe	GTC Val	CAG Gln	CGC Arg	TCC Ser 515	GGA Gly	AAC Asn	TAC Tyr	TTT Phe	GTC Val 520	ACC Thr	1828
ATG Met	TTC Phe	GAT Asp	GAC Asp 525	TAC Tyr	TCA Ser	GCC Ala	ACG Thr	CTG Leu 530	CCA Pro	CTC Leu	ACT Thr	CTC Leu	ATC Ile 535	GTC Val	ATC Ile	1876
CTT Leu	GAG Glu	AAC Asn 540	ATC Ile	GCT Ala	GTG Val	GCC Ala	TGG Trp 545	ATT Ile	TAT Tyr	GGA Gly	CCC Pro	AAG Lys 550	AAG Lys	TTC Phe	ATG Met	1924
CAG Gln	GAG Glu	CTG Leu 555	ACG Thr	GAG Glu	ATG Met 560	CTG Gly	GGC Phe	TTC Arg	CGC Arg	CCC Pro	TAC Tyr 565	CGC Arg	TTC Phe	TAT Tyr	TTC Phe	1972
TAC Tyr 570	ATG Met	TGG Trp	AAG Lys	TTC Phe	GTG Val 575	TCT Ser	CCA Pro	CTA Leu	TGC Cys	ATG Met 580	GCT Met	GTG Ala	CTC Val	ACC Leu	ACA Thr 585	2020
GCC Ala	AGC Ser	ATC Ile	ATC Ile	CAG Gln 590	CTG Leu	GGG Gly	GTC Val	ACG Thr	CCC Pro 595	CCG Pro	GCC Ala	TAC Tyr	AGC Ser	GCC Ala 600	TGG Trp	2068
ATC Ile	AAG Lys	GAG Glu	GAG Ala 605	GCT Ala	GCC Ala	GAG Glu	CGC Arg	TAC Tyr 610	CTG Leu	TAT Tyr	TTC Phe	CCC Pro	AAC Asn 615	TGG Trp	CCC Pro	2116
ATG Met	GCA Ala	CTC Leu 620	CTG Leu	ATC Ile	ACC Thr	CTC Leu	ATC Ile 625	GTC Val	GTG Val	GGC Ala	ACG Thr	CTG Leu 630	CCC Pro	ATC Ile	CCT Pro	2164
GTG Val	GTG Val	TTC Phe 635	GTC Val	CTG Leu	CGG Arg	CAC His 640	TTC Phe	CAC His	CTG Leu	CTC Leu	TCT Ser 645	GAT Asp	GGC Gly	TCC Ser	AAC Asn	2212
ACC Thr 650	CTC Leu	TCC Ser	GTG Val	TCC Ser 655	TAC Tyr	AAG Lys	AAG Lys	Ala	CGC Arg 660	ATG Met	ATG Met	AAG Lys	GAC Asp	ATC Ile	TCC Ser 665	2260
AAC Asn	CTG Leu	GAG Glu	GAG Glu	AAC Asn 670	GAT Asp	GAG Leu	ACC Thr	CGC Arg 675	TTC Phe	ATC Ile	CTC Leu	AGC Ser	AAG Lys	GTG Val 680	CCC Pro	2308
AGT Ser	GAG Glu	GCA Ala	CCT Pro 685	TCC Ser	CCC Pro	ATG Met	CCC Pro	ACT Thr 690	CAC His	CGT Arg	TCC Ser	TAT Tyr	CTG Leu 695	GGG Gly	CCC Pro	2356
GGC Gly	AGC Ser	ACA Thr 700	TCA Ser	CCC Pro	CTG Leu	GAG Glu	ACC Thr 705	AGC Ser	TGG Trp	AAC Asn	CCC Pro	AAT Asn 710	GGA Gly	CCC Pro	TAT Tyr	2404
GGG Gly 715	CGC Arg	GGC Gly	TAC Tyr	CTG Leu	CTG Leu	GCC Ala 720	AGC Ser	ACC Thr	CCT Pro	GAG Glu	TCT Ser 725	GAG Glu	CTG Leu			2446
TGACCACTGC CCAAGCCCAT GCCCGTCTC CCCCCACCG																2485

Val	Thr	Pro	Pro	Ala	Tyr	Ser	Ala	Trp	Ile	Lys	Glu	Glu	Ala	Ala	Gl
		595					600					605			

Arg Tyr Leu Tyr Phe Pro Asn Trp Pro Met Ala Leu Leu Ile Thr Leu
610 615 620

Ile Val Val Ala Thr Leu Pro Ile Pro Val Val Phe Val Leu Arg His
625 630 635 640

Phe His Leu Leu Ser Asp Gly Ser Asn Thr Leu Ser Val Ser Tyr Lys
645 650 655

Lys Ala Arg Met Met Lys Asp Ile Ser Asn Leu Glu Glu Asn Asp Glu
660 665 670

Thr Arg Phe Ile Leu Ser Lys Val Pro Ser Glu Ala Pro Ser Pro Met
675 680 685

Pro Thr His Arg Ser Tyr Leu Gly Pro Gly Ser Thr Ser Pro Leu Glu
690 695 700

Thr Ser Trp Asn Pro Asn Gly Pro Tyr Gly Arg Gly Tyr Leu Leu Ala
705 710 715 720

Ser Thr Pro Glu Ser Glu Leu
725

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACTAAAGCT TGGCATCAAT GCCGAAGAAC

30

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAACTTCTAG AGCAGTGGTC ACAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTAAGATC TGCCACCATG CGAAGAACA GCAAAGTG

38

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAACTGATAT CGCAGTGGTC ACAGCTCAG

29

108000 11112160